OM nucleic - nucleic search, using sw model

Run on: December 30, 2005, 11:17:00 ; Search time 75.3846 Seconds
                                    (without alignments)
                                    471.598 Million cell updates/sec

Title: US-10-623-880-27
Perfect score: 20
Sequence: 1 ccgggcgagggatttctctt 20

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
                2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
                3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
                6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
                8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
                9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

Untitled

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OM nucleic - nucleic search, using sw model

Run on: December 30, 2005, 13:46:17 ; Search time 75.3846 Seconds
                                              (without alignments)
                                              471.598 Million cell updates/sec

Title: US-10-623-880-27
Perfect score: 20
Sequence: 1 ccgggcgagggatttctctt 20

Scoring table: OLIGO_NUC
                  Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size :   0

Total number of hits satisfying chosen parameters: 2546670

Minimum DB seq length: 15
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Issued_Patents_NA:*
                  1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
                  2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
                  3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                  4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                  5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
                  6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                  7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
                  8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
                  9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

Untitled

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OM nucleic - nucleic search, using sw model

Run on: December 30, 2005, 11:17:00 ; Search time 71.6154 Seconds
                                              (without alignments)
                                              471.598 Million cell updates/sec

Title: US-10-623-880-1
Perfect score: 19
Sequence: 1 tccgtaggtgaacctgcgg 19

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
                 8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
                 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

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OM nucleic - nucleic search, using sw model

Run on: December 30, 2005, 13:46:17 ; Search time 71.6154 Seconds
                                           (without alignments)
                                           471.598 Million cell updates/sec

Title: US-10-623-880-1
Perfect score: 19
Sequence: 1 tccgtaggtgaacctgcgg 19

Scoring table: OLIGO_NUC
                Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size :   0

Total number of hits satisfying chosen parameters: 2546670

Minimum DB seq length: 15
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Issued_Patents_NA:*
                1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
                2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
                3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
                6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
                8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
                9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.